

II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

1. Full-length PRO213 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO213. In particular, Applicants have identified and isolated cDNA encoding a PRO213 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that a portion of the PRO213 polypeptide has significant homology with the human growth arrest-specific 6 (gas6) protein. Accordingly, it is presently believed that PRO213 polypeptide disclosed in the present application may have the same or similar activity as does the gas6 protein.

2. Full-length PRO274 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO274. In particular, Applicants have identified and isolated cDNA encoding a PRO274 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO274 polypeptide have significant homology with the 7 transmembrane segment receptor proteins and Fn54 protein. Accordingly, it is presently believed that PRO274 polypeptide disclosed in the present application is a newly identified member of the 7 transmembrane segment receptor protein and/or Fn54 protein family.

3. Full-Length PRO300 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO300. In particular, Applicants have identified and isolated cDNA encoding a PRO300 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA

sequence alignment computer programs, Applicants found that various portions of the PRO300 polypeptide have significant homology with the human Diff 33 protein. Accordingly, it is presently believed that PRO300 polypeptide disclosed in the present application is a newly identified member of the Diff 33 family.

4. **Full-length PRO284 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO284. In particular, Applicants have identified and isolated cDNA encoding a PRO284 polypeptide, as disclosed in further detail in the Examples below. To Applicants present knowledge, the UNQ247 (DNA23318-1211) nucleotide sequence encodes a novel factor; using BLAST and FastA sequence alignment computer programs, no sequence identities to any known proteins were revealed.

5. **Full-length PRO296 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO296. In particular, Applicants have identified and isolated cDNA encoding a PRO296 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO296 polypeptide has significant similarity to the sarcoma-amplified SAS protein. Accordingly, it is presently believed that PRO296 polypeptide disclosed in the present application is a newly identified SAS protein homolog.

6. **Full-length PRO329 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO329. In particular, Applicants have identified and isolated cDNA encoding a PRO329 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO329 polypeptide has significant similarity to a high affinity immunoglobulin F_c receptor. Accordingly, it is presently believed that PRO329 polypeptide disclosed in the present application is a newly identified F_c receptor homolog.

7. **Full-length PRO362 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO362. In particular, Applicants have identified and isolated cDNA encoding a PRO362 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO362 polypeptide has significant similarity to the A33 antigen protein as well as the HCAR protein and the NrCAM related cell adhesion molecule. Accordingly, it is presently believed that PRO362 polypeptide disclosed in the present application is a newly A33 antigen and HCAR protein homolog.

8. **Full-length PRO363 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides

referred to in the present application as PRO363. In particular, Applicants have identified and isolated cDNA encoding a PRO363 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO363 polypeptide has significant similarity to the cell surface protein HCAR. Accordingly, it is presently believed that PRO363 polypeptide disclosed in the present application is a newly HCAR homolog.

9. **Full-length PRO868 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO868. In particular, Applicants have identified and isolated cDNA encoding a PRO868 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO868 polypeptide has significant similarity to the tumor necrosis factor receptor. Accordingly, it is presently believed that PRO868 polypeptide disclosed in the present application is a newly identified member of the tumor necrosis factor receptor family of proteins.

10. **Full-length PRO382 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO382. In particular, Applicants have identified and isolated cDNA encoding a PRO382 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the native PRO382 polypeptide shares significant homology with various serine protease proteins. Applicants have also found that the DNA encoding the PRO382 polypeptide shares significant homology with nucleic acid encoding various serine protease proteins. Accordingly, it is presently believed that PRO382 polypeptide disclosed in the present application is a newly identified serine protease homolog.

11. **Full-length PRO545 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO545. In particular, Applicants have identified and isolated cDNA encoding a PRO545 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO545 polypeptide have significant homology with the sequences identified designated as; human metalloproteinase ("P_W01825"), mouse meltrin alpha ("S60257"), metalloprotease-disintegrin meltrin-alpha ("GEN13695"), ADAM 13 - *Xenopus laevis* ("XLU66003_1"), mouse meltrin beta ("S60258"), rabbit metalloprotease-disintegrin meltrin-beta, ("GEN13696"), human meltrin S ("AF023477_1"), human meltrin precursor ("AF023476_1"), human ADAM 21 ("AF029900_1"), and human ADAM 20 ("AF029899_1"), thereby indicating that PRO545 may be a novel meltrin protein. Accordingly, it is presently believed that the PRO545 polypeptide disclosed in the present application is a newly identified member of the meltrin family and possesses the cellular adhesiveness typical of the meltrin proteins which comprise both metalloprotease and disintegrin domains.

12. **Full-length PRO617 Polypeptides**